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Ehlich, Andreas
Bohlen, Heribert
Schwengberg, Silke

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<141> 2004-07-08

<150> PCT/EP04/07529

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<223> pUC plasmid replication origin

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<222> (9401) .. (9406)

<223> Herpes simplex virus thymidine kinase polyadenylation signal

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<222> (9414) .. (9419)

<223> Herpes simplex virus thymidine kinase polyadenylation signal

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<221> terminator

<222> (9163) .. (9165)

<223> Kanamycin/neomycin resistance gene

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<221> ATG

<222> (8371) .. (8373)

<223> Kanamycin/neomycin resistance gene

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<221> promoter

<222> (8242) .. (8248)

<223> SV40 early promoter element

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<222> (8167) .. (8230)

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Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn Glu Val Ile Ser Val Met				
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Asn Arg Ala Lys Lys Ala Gly Lys Ser Val Gly Val Val Thr Thr Thr				
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Arg Val Gln His Ala Ser Pro Ala Gly Thr Tyr Ala His Thr Val Asn				
cgc aac tgg tac tcg gac gcc gac gtg cct gcc tcg gcc cgc cag gag	185	190	195	6151
Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro Ala Ser Ala Arg Gln Glu				
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Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile Ser Asn Met Asp Ile Asp				
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Val Ile Leu Gly Gly Arg Lys Tyr Met Phe Arg Met Gly Thr Pro				
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Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln Gly Gly Thr Arg Leu Asp				
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Gly Lys Asn Leu Val Gln Glu Trp Leu Ala Lys Arg Gln Gly Ala Arg				
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Tyr Val Trp Asn Arg Thr Glu Leu Met Gln Ala Ser Leu Asp Pro Ser				
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Val Thr His Leu Met Gly Leu Phe Glu Pro Gly Asp Met Lys Tyr Glu				
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Ile His Arg Asp Ser Thr Leu Asp Pro Ser Leu Met Glu Met Thr Glu				
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Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro Arg Gly Phe Phe Leu Phe				
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Val Glu Gly Gly Arg Ile Asp His Gly His His Glu Ser Arg Ala Tyr				
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10	15

Gly Ile Ile Pro Val Glu Glu Asn Pro Asp Phe Trp Asn Arg Glu	
20	25
30	

Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr	
35	40
45	

Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser

50

55

60

Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu
 65 70 75 80

Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu
 85 90 95

Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr
 100 105 110

Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly
 115 120 125

Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn
 130 135 140

Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val
 145 150 155 160

Gly Val Val Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr
 165 170 175

Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro
 180 185 190

Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile
 195 200 205

Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly Arg Lys Tyr Met
 210 215 220

Phe Arg Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln
 225 230 235 240

Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala
 245 250 255

Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln
 260 265 270

Ala Ser Leu Asp Pro Ser Val Thr His Leu Met Gly Leu Phe Glu Pro
 275 280 285

Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser Thr Leu Asp Pro Ser
 290 295 300

Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro
305 310 315 320

Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His
325 330 335

His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu Thr Ile Met Phe Asp
340 345 350

Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser Glu Glu Asp Thr Leu
355 360 365

Ser Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr
370 375 380

Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Arg
385 390 395 400

Asp Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly Asn Gly Pro Gly Tyr
405 410 415

Val Leu Lys Asp Gly Ala Arg Pro Asp Val Thr Glu Ser Glu Ser Gly
420 425 430

Ser Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro Leu Asp Glu Glu Thr
435 440 445

His Ala Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His
450 455 460

Leu Val His Gly Val Gln Glu Gln Thr Phe Ile Ala His Val Met Ala
465 470 475 480

Phe Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys Asp Leu Ala Pro Pro
485 490 495

Ala Gly Thr Thr Asp Ala Ala His Pro Gly Tyr Ser Arg Val Gly Ala
500 505 510

Ala Gly Arg Phe Glu Gln Thr
515